

SEQUENCE LISTING

<110> Itadani, Hiraku
 Takimura, Tetsuo
 Nakamura, Takao
 Kobayashi, Masahiko
 Tanaka, Ken-ichi
 Hidaka, Yusuke
 Ohta, Masataka

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)
 BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

<130> 06501-083001

<140> 09/891,053

<141> 2001-06-25

<150> PCT/JP99/07280

<151> 1999-12-24

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 11/145661

<151> 1999-05-25

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 413

<212> PRT

<213> Rattus norvegicus

<400> 1

```

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1           5           10           15
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
      20           25           30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
      35           40           45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
      50           55           60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
      65           70           75           80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
      85           90           95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
      100          105          110
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
      115          120          125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

```

130 135 140
 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
 145 150 155 160
 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
 165 170 175
 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
 180 185 190
 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
 195 200 205
 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
 210 215 220
 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
 225 230 235 240
 Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Ala Pro Pro
 245 250 255
 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
 260 265 270
 His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
 275 280 285
 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
 290 295 300
 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
 305 310 315 320
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
 325 330 335
 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
 340 345 350
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
 355 360 365
 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
 370 375 380
 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
 385 390 395 400
 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
 405 410

<210> 2
 <211> 1239
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)...(1239)

<400> 2
 atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 48
 Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1 5 10 15
 gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 96
 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30
 tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 144
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser 50 55 60	192
ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp 65 70 75 80	240
ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu 85 90 95	288
acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val 100 105 110	336
gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile 115 120 125	384
agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala 130 135 140	432
cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp 145 150 155 160	480
gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr 165 170 175	528
ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe 180 185 190	576
ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe 195 200 205	624
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn 210 215 220	672
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly 225 230 235 240	720
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro 245 250 255	768
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu 260 265 270	816

cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc	864
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu	
275 280 285	
aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc	912
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg	
290 295 300	
atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg	960
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg	
305 310 315 320	
gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg	1008
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly	
325 330 335	
ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc	1056
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys	
340 345 350	
cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt	1104
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu	
355 360 365	
ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac	1152
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His	
370 375 380	
tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc	1200
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu	
385 390 395 400	
aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag	1239
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys	
405 410	

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(21)

<223> n = A,T,C or G

<400> 3

batngccaac ctbkcocttct c

21

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 4

ccataaaagn nggggttgac

20

<210> 5

<211> 2700

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (351)...(1589)

<221> misc_feature

<222> (1)...(2700)

<223> n = A,T,C or G

<400> 5

aattcggcac	gagcgggcag	atcgcggggc	gcactcggtt	gcgcgctgag	ctaggggtgc	60
accgacgcac	cgcgggcggc	tggagctcgg	ctttgctctc	gctgcagcag	ccgcgccgcc	120
cgccccactc	cgctcagatt	ccgacaccag	ccccctctgg	atcgccctcc	tggactctag	180
cccgggctct	tgtccgacc	ccgcggacca	tgtccgggc	gcccccgga	aaaccgggct	240
gggcgaagag	ccggcaaaga	ttaggtcac	gagcgggggc	cccaccggc	caccagctc	300
tccgcccgtg	ccctgcccg	tgtccccgag	ccgtgtgagc	ctgctgggcc	atg gag	356
					Met Glu	
					1	

cgc gcg ccg	ccc gac	ggg ctg	atg aac	gcg tcg	ggc act	ctg gcc	gga	404
Arg Ala Pro	Pro Asp Gly	Leu Met Asn	Ala Ser Gly	Thr Leu Ala	Gly			
5		10		15				

gag gcg gcg	gct gca	ggc ggg	gcg cgc	ggc ttc	tcg gct	gcc tgg	acc	452
Glu Ala Ala	Ala Ala Gly	Gly Ala Arg	Gly Phe Ser	Ala Ala Trp	Thr			
20		25		30				

gct gtc ctg	gct gcg	ctc atg	gcg ctg	ctc atc	gtg gcc	aca gta	ctg	500
Ala Val Leu	Ala Ala Leu	Met Ala Leu	Leu Ile Val	Ala Thr Val	Leu			
35		40		45		50		

ggc aac gcg	ctg gtc	atg ctc	gcc ttc	gtg gcg	gat tcg	agc ctc	cgc	548
Gly Asn Ala	Leu Val Met	Leu Ala Phe	Val Ala Asp	Ser Ser Leu	Arg			
55		60		65				

acc cag aac	aac ttc	ttt ctg	ctc aac	ctc gcc	atc tcc	gac ttc	ctc	596
Thr Gln Asn	Asn Phe Phe	Leu Leu Asn	Leu Ala Ile	Ser Asp Phe	Leu			
70		75		80				

gtg ggt gcc	ttc tgc	atc cca	ttg tac	gta ccc	tat gtg	ctg acc	ggc	644
Val Gly Ala	Phe Cys Ile	Pro Leu Tyr	Val Pro Tyr	Val Leu Thr	Gly			
85		90		95				

cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp 100 105 110	692
tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr 115 120 125 130	740
gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln 135 140 145	788
ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu 150 155 160	836
gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser 165 170 175	884
ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr 180 185 190	932
aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro 195 200 205 210	980
ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln 215 220 225	1028
agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu 230 235 240	1076
ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys 245 250 255	1124
tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser 260 265 270	1172
tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc aaa agg Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg 275 280 285 290	1220
ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc atg aag Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg Met Lys 295 300 305	1268
atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg gac aag Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg Asp Lys 310 315 320	1316
aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg ctc tgc	1364

Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys
 325 330 335

tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc cat ggc 1412
 Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys His Gly
 340 345 350

cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt ctg tgg 1460
 Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp
 355 360 365 370

gcc aac tgc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc 1508
 Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser
 375 380 385

ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc 1556
 Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val
 390 395 400

cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgagcagctg cccaccctt 1609
 Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
 405 410

ctgaggccag gcccttgtag ttgtttgagt gggcagccgg agcgtgggag gggccctggg 1669
 ccatgctccg ctccaaatgc catggcgccg tcttagatca tcaaccccg agtggggtag 1729
 catggcaggt gggccaagag ccctagttgg tggagctaga gtgtgctggt tagctctgcc 1789
 gccacattct ccttcaccac acagaagaga caatccagga gtcccaggca tgccttcac 1849
 ctacacacac acacacacac acacacacac acacaccaca gtgcagtgcc agtgatgtcc 1909
 ccttttgcag atttagtggt tgggtgtcct cctaattgcaa acctcggtgt gtgctcccg 1969
 ctccggccct ggcaatgcgt gcgtgcgccc tgcattgtgt cacaccgccc acacaccgc 2029
 ccgccacaca cttgcaacac ctccctctct ccagaagagc tggggacgat gccctttgct 2089
 gccactgtct cttgcttaat ccagagccct ggctccttat cccccactct cccttcaact 2149
 ctgccccaca aagtgtcgag cgctcgga aacttgaagc ttctctgtct ctccactct 2209
 ggatgttttc aggaagatgg aggagaagaa aacacgtctg tgaacttgat gttccttgga 2269
 tgtttaatca agagagacaa aattgccgag gagctcgggg ctggattggc aggtgtggg 2329
 tcccacgccc tccctccctca gtgctgcagc ttccggctga gccgcgccag ctgcttctgc 2389
 ctgccccgcc ccagagcttg ggacgatggc cctgccctgc ttgccccgtc tgtacaatca 2449
 gaatttgggg gtgggtggtt atggggtaga gcggctcttc actgtgccct aaaggtcctg 2509
 aggtcacag gacagtcagc aggagagcag gcaggccgc gacacctggg aggaatgctt 2569
 tgcctcgctc tgtgtactca cctcaggctt ctgcattgtc tgctgccctt gtgccctgg 2629
 gtgctgcctc tgccaatgtg aaaacacaat aaagtgtatt tttttacgga aaaaaaana 2689
 aaaaaaaaa a 2700

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> artificially synthesized primer sequence

<400> 6
 cgaggatccg tgaggctccg gtgcccgtc 29

<210> 7
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 7

cgggtaagct tcacgacacc tgaaatggaa ga

32

<210> 8

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 8

ccttctgcat cccattgtac gtacc

25

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 9

cttccgccgg gccttcacca a

21

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 10

acagacacgg cggggctcac

20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (280) ... (557)

<221> misc_feature

<222> (1) ... (1350)

<223> n = A,T,C or G

<400> 11

gcactcggct ggcggttgcn tccggctgca cggtcgcacc ggcagcggct caggctccgg
ctcctctccc gctgcagcag ccgcgctgcc ggccccactg ggctcggatc cggccccggc

60

120


```

ccccctcggca ccgcctgctc tggccccggc cccggccccg cggaccatgc gctgggcgcc 190
cccaggggaa cccgacccgg ccaagggccc gcaaagacga ggctcccggg ccggggcccc 240
tccccggccgc ccagctctcg gccggcgccc tgcccccgct cccggagccg cgtgagcctg 300
cggggccatg gagcgcgcgc cgcccagcgg gccgctgaac gcttcggggg cgtggcggg 360
cgaggcggcg gcggcggggc gggcgcgcgg cttctcggca gcctggaccg cgggtgctggc 420
cgcgctcatg gcgtgctca tcgtggccac ggtgctgggc aacgcgctgg tcatgctgc 480
cttcgtggcc gactcgagcc tccgcacca gaacaacttc ttcctgctca acctcgccat 540
ctccgacttc ctcgtcggta aatccccagc ccttgccgc tggggaccca ggggcgcccc 600
gcgtggccgg gccagcgggg actggaacac ggacctgggt ggctcccga ggacacgcc 660
ccaccagggg acccggcctg ggaagggggc gtccggagcc catggggtgg ggggcacagg 720
cgaagtccct tgccactcag gcctcgggac aggggctggg gagagatgtc cccgggaagg 780
gacacgggca ctgggcgagg cgcaaggcgc aaaggcagcg ggtgcagctc tggctcctgc 840
gctgtagcca aacaaaggct gctgcggaact taggacgcgc ggagggcgca gtggggcggt 900
ttagagaagg tctgggggag gggacatgga agggggattt ttagagctgt gttgggggaa 960
gggacgggtg ggaaggtggg ggttggggga gacgctcgga ggagcgtgct ctacgtgtc 1020
caggctctgc tgccggctgg ggggcggggc acgcggaggg ggctggagcg ccagacacct 1080
gttggggctg tgaggtgctg ctcccagacg ctccaagccc gcttggcagt agtagtagcg 1140
gctggcggct ggcgctgca accaagtgcc ctttcagcca ggagaaaggc tttctccttg 1200
tctaagctga gaccgagggg tgtccagcgc cagggtaggg gctggagtcc agcgggggag 1260
gggagaagga aattgtcttc tttctcctt tgagggctgg gagggctgga cagaagtcca 1320
gggaatcccg actccaggtc ctcgggggtc 1350

```

```

<210> 12
<211> 448
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> exon
<222> (259) ... (425)

```

```

<400> 12
gagctcccca tgcttggatc atccctcctg cccccaggcc caggggacac agatagtgtc 60
gggagctatg tgggggtgaa ggctggcgcc agggcagagt ttgtggctga caccaggtgg 120
aggggtggta agatgaggat ggctagtctc agaaaagcag ccaccatgtg acccaggtc 180
ccgccggtgt ctgcgttag gtccgtctgt cccctggccc ctggctgcat ggtcccactg 240
tggccctact cccacagggc gccttctgca tccactgta tgtaccctac gtgctgacag 300
gccgctggac cttcgccggg ggctctgca agctgtggct ggtagtggac tacctgtgt 360
gcacctctc tgcttcaac atcgtgctca tcagctacga ccgcttctg tcggtcacc 420
gagcggtagg tcttgggctg cggagctc 448

```

```

<210> 13
<211> 1893
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> exon
<222> (293) ... (1209)

```

```

<400> 13
gagctcacag ctggtagggg gtggtaaaca ggcagcctag cagagagtga gggttcaggt 60
tgggtccagg gagcttctga ggctctcact gagtgtggca gggcaccagt ccgggacccc 120
agtggggagg gtttagaggaa gggaggggaa agagggaggg agggaggaca ggaggggaaa 180
ggaggagcat tgctgctgag ggaagggccc acataggggc ccacaggcta cgggggcgca 240
cccagcccaa tattccttcc gccccgcccc tgaccagcct gcccttctgc aggtctcata 300
ccgggcccag caggggtgaca cgcggcgggc agtgcggaag atgctgctgg tgtgggtgct 360

```

```

ggccttctctg ctgtacggac cagccatcct gagctgggag tacctgtccg ggggcagctc 420
catccccgag ggccactgct atgccgagtt cttctacaac tgggtacttcc tcatcacggc 480
ttccaccctg gagttcttta cgcccttctc cagcgtracc ttctttaacc tcagcatcta 540
cctgaacatc cagaggcgca cccgcctccg gctggatggg gctcgagagg cagccggccc 600
cgagccccct cccgaggccc agccctcacc acccccaccg cctggctgct ggggctgctg 660
gcagaagggg cacggggagg ccatgccgct gcacaggtat ggggtgggtg aggcggccgt 720
aggcgctgag gccggggagg cgaccctcgg ggggtggcgg gggggcggtt ccgtggcttc 780
accacactcc agctccggca gtcctcagag gggcactgag aggcgcgct cactcaagag 840
gggctccaag ccatcgccgt cctcgccctc actggagaag cgcatgaaga tgggtgtcca 900
gagcttcacc cagcgctttc ggctgtctcg ggacaggaaa gtggccaagt cgctggccgt 960
catcgtgagc atctttgggc tctgctgggc ccatacacg ctgctgatga tcatccgggc 1020
cgcctgccat ggccactgcg tccctgacta ctggtacgaa acctccttct ggctcctgtg 1080
ggccaactcg gctgtcaacc ctgtcctcta cctctgtgct caccacagct tccgccgggc 1140
cttcaccaag ctgctctgcc ccagaaagct caaaatccag cccacagct ccctggagca 1200
ctgctggaag tgagtggccc accagagcct ccctcagcca cgcctctctc agcccaggtc 1260
tcctgggcat ctggccctgc tgccccctac ccggctcgtt ccccagggg tgagccccgc 1320
cgtgtctgtg gccctctctt aatgccacgg cagccaccct gccatggagg cgccttctctg 1380
ggttggccag agggccctc actggctgga ctggaggctg ggtggccggc cctgcccccc 1440
acattctggc tccaccggga gggacagtct ggagggtcca gacatgctgc ccacccccctg 1500
ctgggtgcca cccttcgag ttactgggtg gtgttcttcc caaagcaagc acctgggtgt 1560
gctccaggct tcctgcccta gcagtttgcc tctgcacgtg cacacacctg cacacccctg 1620
cacacacctg cacaccgtcc ctctccccgg acaagcccag gacactgcct ttgctgcctt 1680
ctgtctcttg cataagcctc aggcctggcc ctttcacccc tcttcccacc aactctctct 1740
gccccaaaaa gtgtcaaggg gccctaggaa cctcgaagct gttctctgct tttccattct 1800
gggtgttttc agaaagatga agaagaaaac atgtctgtga acttgatgtt cctgggatgt 1860
ttaatcaaga gagacaaaat tgctgaggag ctc 1893

```

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 14

tgaacgcttc gggggcgctg

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 15

gagatggcga ggttgagcag g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 16
ggctccaagc catcggcgtc 20

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 17
ctcacttcca gcagtgtcc 20

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 18
gcctccgcac ccagaacaac 20

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<400> 19
tgcgctctg gatgttcag 19

<210> 20
<211> 453
<212> PRT
<213> Homo sapiens

<400> 20
Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu
1 5 10 15
Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
20 25 30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
35 40 45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
50 55 60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
85 90 95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
100 105 110
Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

```

      115              120              125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
      130              135              140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp
      145              150              155              160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
      165              170              175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
      180              185              190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
      195              200              205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
      210              215              220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala
      225              230              235              240
Gly Pro Glu Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro Pro
      245              250              255
Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu
      260              265              270
His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu
      275              280              285
Ala Thr Leu Gly Gly Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr
      290              295              300
Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
      305              310              315              320
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
      325              330              335
Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg
      340              345              350
Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly
      355              360              365
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
      370              375              380
His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
      385              390              395              400
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
      405              410              415
His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
      420              425              430
Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys
      435              440              445
Lys Lys Thr Cys Leu
      450

```

<210> 21

<211> 2050

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271)...(1629)

<400> 21

```

agagatgtag ggcgccccctt ttagctgctg acagaacgaa agaactcggt ttttctttaa      60
gtgagtgtgc ttgggtgacg cttagggcgc cctccgcagt gcgcgcagga aagcgcaactg      120
aggctgcgga ggcagagctg catgctgggt gcggaagag gtgggctccg tcgcggagtc      180

```

gctgagtc	ccg	tgccctttta	gttagttctg	cagtcctagta	tggtcccat	ttgcccttcc	240
actcccg	gag	ccgcgtgagc	ctgcggggcc	atg	gag	cgc gcg ccg ccc gac ggg	294
				Met	Glu	Arg Ala Pro Pro Asp Gly	
				1		5	
ccg	ctg	aac	gct	tcg	ggg	gcg	342
Pro	Leu	Asn	Ala	Ser	Gly	Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly	
	10				15	20	
ggg	gcg	cgc	ggc	ttc	tcg	gca	390
Gly	Ala	Arg	Gly	Phe	Ser	Ala Ala Trp Thr Ala Val Leu Ala Ala Leu	
	25				30	35	40
atg	gcg	ctg	ctc	atc	gtg	gcc	438
Met	Ala	Leu	Leu	Ile	Val	Ala Thr Val Leu Gly Asn Ala Leu Val Met	
				45		50	55
ctc	gcc	ttc	gtg	gcc	gac	tcg	486
Leu	Ala	Phe	Val	Ala	Asp	Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe	
			60			65	70
ctg	ctc	aac	ctc	gcc	atc	tcc	534
Leu	Leu	Asn	Leu	Ala	Ile	Ser Asp Phe Leu Val Gly Ala Phe Cys Ile	
		75				80	85
cca	ctg	tat	gta	ccc	tac	gtg	582
Pro	Leu	Tyr	Val	Pro	Tyr	Val Leu Thr Gly Arg Trp Thr Phe Gly Arg	
	90					95	100
ggc	ctc	tgc	aag	ctg	tgg	ctg	630
Gly	Leu	Cys	Lys	Leu	Trp	Leu Val Val Asp Tyr Leu Leu Cys Thr Ser	
	105				110	115	120
tct	gcc	ttc	aac	atc	gtg	ctc	678
Ser	Ala	Phe	Asn	Ile	Val	Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val	
			125			130	135
acc	cga	gcg	gtc	tca	tac	cgg	726
Thr	Arg	Ala	Val	Ser	Tyr	Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala	
			140			145	150
gtg	cgg	aag	atg	ctg	ctg	gtg	774
Val	Arg	Lys	Met	Leu	Leu	Val Trp Val Leu Ala Phe Leu Leu Tyr Gly	
		155				160	165
cca	gcc	atc	ctg	agc	tgg	gag	822
Pro	Ala	Ile	Leu	Ser	Trp	Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro	
	170					175	180
gag	ggc	cac	tgc	tat	gcc	gag	870
Glu	Gly	His	Cys	Tyr	Ala	Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile	
	185				190	195	200
acg	gct	tcc	acc	ctg	gag	ttc	918
Thr	Ala	Ser	Thr	Leu	Glu	Phe Phe Thr Pro Phe Leu Ser Val Thr Phe	
			205			210	215

ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg	966
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg	
220 225 230	
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc	1014
Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Glu Ala	
235 240 245	
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag	1062
Gln Pro Ser Pro Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys	
250 255 260	
ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg	1110
Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala	
265 270 275 280	
gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg	1158
Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly Gly	
285 290 295	
ggc ggc tcc gtg gct tca ccc acc tcc agc tcc ggc agc tcc tcg agg	1206
Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg	
300 305 310	
ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg	1254
Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala	
315 320 325	
tcc tcg gcc tcg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc	1302
Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe	
330 335 340	
acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg	1350
Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu	
345 350 355 360	
gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg	1398
Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu	
365 370 375	
ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac	1446
Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr	
380 385 390	
tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac	1494
Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn	
395 400 405	
cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc	1542
Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr	
410 415 420	
aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg	1590
Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu	
425 430 435 440	
gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat	1639

Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu
 445 450

```

gttcctggga tgtttaatca agagagacaa aattgctgag gagctcaggg ctggattggc 1699
aggtgtgggc tcccacgccc tcctccctcc gctaaggctt ccggctgagc tgtgccagct 1759
gcttctgccc acccgcctc tgggctcaca ccagccctgg tggccaagcc tgccccggcc 1819
actctgtttg ctacaccagg acctctgggg gttgttggga ggagggggcc cggtggggcc 1879
cgaggggtccc aaggcgtgca ggggcggtcc agaggaggtg cccgggcagg ggccgcttcg 1939
ccatgtgctg tgcaccctg ccacgcgctc tgcattgctc tctgctgtg cccgctgcgc 1999
tgccctgcaa accgtgaggt cacaataaag tgtatttttt tattggtgct g 2050

```

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 22

tgcattcccat tgtacgtncc

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 23

atcattagga gcgtgtangg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 24

tgctctggga caccatcttc

20

<210> 25

<211> 445

<212> PRT

<213> Rattus norvegicus

<400> 25

Met	Glu	Arg	Ala	Pro	Pro	Asp	Gly	Leu	Met	Asn	Ala	Ser	Gly	Thr	Leu
1				5				10						15	
Ala	Gly	Glu	Ala	Ala	Ala	Ala	Gly	Gly	Ala	Arg	Gly	Phe	Ser	Ala	Ala
			20					25					30		
Trp	Thr	Ala	Val	Leu	Ala	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr
		35					40					45			
Val	Leu	Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser
	50					55					60				
Leu	Arg	Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp
65				70						75				80	
Phe	Leu	Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu
			85					90						95	
Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val
			100					105					110		
Val	Asp	Tyr	Leu	Leu	Cys	Ala	Ser	Ser	Val	Phe	Asn	Ile	Val	Leu	Ile
		115						120				125			
Ser	Tyr	Asp	Arg	Phe	Leu	Ser	Val	Thr	Arg	Ala	Val	Ser	Tyr	Arg	Ala
	130					135					140				
Gln	Gln	Gly	Asp	Thr	Arg	Arg	Ala	Val	Arg	Lys	Met	Ala	Leu	Val	Trp
145				150						155				160	
Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr
			165					170						175	
Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe
		180						185					190		
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe
		195				200						205			
Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn
	210					215					220				
Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly
225				230						235				240	
Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro
				245					250					255	
Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu
		260						265					270		
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu
	275						280					285			
Ala	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ala	Ala	Ala	Ser	Pro	Thr
	290					295					300				
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu
305				310						315				320	
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg
				325					330					335	
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg
		340						345					350		
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly
	355						360					365			
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys
	370					375					380				
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu
385				390						395				400	
Leu	Trp	Ala	Asn	Ser	Ala	Val	Asn	Pro	Val	Leu	Tyr	Pro	Leu	Cys	His
			405						410					415	
Tyr	Ser	Phe	Arg	Arg	Ala	Phe	Thr	Lys	Leu	Leu	Cys	Pro	Gln	Lys	Leu
		420						425					430		
Lys	Val	Gln	Pro	His	Gly	Ser	Leu	Glu	Gln	Cys	Trp	Lys			
	435						440					445			

<210> 26
 <211> 1953
 <212> DNA
 <213> *Rattus norvegicus*

<220>
 <221> CDS
 <222> (302)...(1636)

<400> 26
 agctaggggt gcaccgacgc accgcggcgg ctggagctcg gctttgctct cgctgcagca 60
 gccgcgccgc ccgcccact ccgctcagat tccgacacca gcccctctg gatcgccctc 120
 ctggactcta gcccgggctc ttgctccgac ccgcgggacc atgctccggg cgcgccccgg 180
 aaaaccgggc tgggcgaaga gccggcaaaag attaggctca cgagcggggg ccccaccgg 240
 ccaccagct ctccgcccg gtccgtgccg gtgtcccgga gccgtgtgag cctgctgggc 300
 c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 349
 Met Glu Arg Ala Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1 5 10 15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 397
 Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 445
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc 493
 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 541
 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 589
 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg 637
 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 100 105 110

gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc 685
 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
 115 120 125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 733
 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
 130 135 140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg 781
 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
 145 150 155 160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 829

Val	Leu	Ala	Phe	Leu	Leu	Tyr	Gly	Pro	Ala	Ile	Leu	Ser	Trp	Glu	Tyr	
			165						170					175		
ctg	tct	ggg	ggc	agt	tcc	atc	ccc	gag	ggc	cac	tgc	tat	gct	gag	ttc	877
Leu	Ser	Gly	Gly	Ser	Ser	Ile	Pro	Glu	Gly	His	Cys	Tyr	Ala	Glu	Phe	
			180					185					190			
ttc	tac	aac	tgg	tac	ttt	ctc	atc	acg	gcc	tcc	acc	ctc	gag	ttc	ttc	925
Phe	Tyr	Asn	Trp	Tyr	Phe	Leu	Ile	Thr	Ala	Ser	Thr	Leu	Glu	Phe	Phe	
		195					200					205				
acg	ccc	ttc	ctc	agc	gtt	acc	ttc	ttc	aac	ctc	agc	atc	tac	ctg	aac	973
Thr	Pro	Phe	Leu	Ser	Val	Thr	Phe	Phe	Asn	Leu	Ser	Ile	Tyr	Leu	Asn	
	210					215					220					
atc	cag	agg	cgc	acc	cgc	ctt	cgg	ctt	gat	ggg	ggc	cgt	gag	gct	ggc	1021
Ile	Gln	Arg	Arg	Thr	Arg	Leu	Arg	Leu	Asp	Gly	Gly	Arg	Glu	Ala	Gly	
225					230				235						240	
cca	gaa	ccc	cca	cca	gat	gcc	cag	ccc	tcg	cca	cct	cca	gct	ccc	ccc	1069
Pro	Glu	Pro	Pro	Pro	Asp	Ala	Gln	Pro	Ser	Pro	Pro	Pro	Ala	Pro	Pro	
			245						250					255		
agc	tgc	tgg	ggc	tgc	tgg	cca	aaa	ggg	cat	ggc	gag	gcc	atg	ccg	ttg	1117
Ser	Cys	Trp	Gly	Cys	Trp	Pro	Lys	Gly	His	Gly	Glu	Ala	Met	Pro	Leu	
			260					265					270			
cac	agg	tat	ggg	gtg	ggg	gag	gca	ggc	cct	ggg	gtt	gag	gct	ggg	gag	1165
His	Arg	Tyr	Gly	Val	Gly	Glu	Ala	Gly	Pro	Gly	Val	Glu	Ala	Gly	Glu	
		275					280					285				
gct	gcc	ctc	ggg	ggg	ggc	agt	ggg	gga	ggg	gct	gct	gcc	tcg	ccc	acc	1213
Ala	Ala	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ala	Ala	Ala	Ser	Pro	Thr	
	290					295					300					
tcc	agc	tct	ggc	agc	tcc	tca	agg	ggc	act	gag	agg	cca	cgc	tca	ctc	1261
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu	
305					310				315						320	
aaa	agg	ggc	tcc	aag	cca	tca	gca	tct	tca	gca	tcc	ctg	gag	aag	cgc	1309
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg	
			325					330						335		
atg	aag	atg	gtg	tcc	cag	agc	atc	acc	cag	cgc	ttc	cgg	ctg	tcg	cgg	1357
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg	
			340					345					350			
gac	aag	aag	gtg	gcc	aag	tcg	ctg	gcc	atc	atc	gtg	agc	atc	ttt	ggg	1405
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly	
		355					360					365				
ctc	tgc	tgg	gcg	ccg	tac	acg	ctc	cta	atg	atc	atc	cga	gct	gct	tgc	1453
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys	
	370					375					380					
cat	ggc	cgc	tgc	atc	ccc	gat	tac	tgg	tac	gag	acg	tcc	ttc	tgg	ctt	1501
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu	

385	390	395	400	
ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac				1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His				
	405	410	415	
tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc				1597
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu				
	420	425	430	
aag gtc cag ccc cac gcc tcc ctg gag cag tgc tgg aag tgagcagctg				1646
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys				
	435	440	445	
ccccaccctt ctgaggccag gcccttgtag ttgtttgagt gggcagccgg agcgtgggag				1706
gggccctggt ccatgctccg ctccaaatgc catggcgcc tcttagatca tcaaccccg				1766
agtgggtag catggcaggt gggccaagag ccctagttgg tggagctaga gtgtgctggt				1826
tagctctgcc gcacattctc cttcaccaca cagaagagac aatccaggag tcccaggcat				1886
gccttcacct acacacacac acacacacac acacacacac acaccacagt gcagtgccag				1946
tgatgtc				1953